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```
RAW SEQUENCE LISTING                    DATE: 06/17/2002
PATENT APPLICATION:  US/10/092,925      TIME: 12:40:29

       Input Set : A:\06501-102US1.TXT
       Output Set: N:\CRF3\06172002\J092925.raw
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 4  <110> APPLICANT: Kitamura, Toshio
 5         Morita, Sumiyo
 7  <120> TITLE OF INVENTION: TSG-LIKE GENE
10  <130> FILE REFERENCE: 06501-102US1
12  <140> CURRENT APPLICATION NUMBER: 10/092,925
13  <141> CURRENT FILING DATE: 2002-06-10
15  <150> PRIOR APPLICATION NUMBER: PCT/JP00/06050
16  <151> PRIOR FILING DATE: 2000-09-06
18  <150> PRIOR APPLICATION NUMBER: JP 11/252190
19  <151> PRIOR FILING DATE: 1999-09-06
21  <160> NUMBER OF SEQ ID NOS: 5
23  <170> SOFTWARE: FastSEQ for Windows Version 4.0
25  <210> SEQ ID NO: 1
26  <211> LENGTH: 3986
27  <212> TYPE: DNA
28  <213> ORGANISM: Mus musculus
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32  <222> LOCATION: (87)...(752)
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36  ctactgagtg acttctttga agaacc atg aag tca cac tat att gtg cta gct    113
37                                 Met Lys Ser His Tyr Ile Val Leu Ala
38                                  1               5
40  cta gcc tcc ctg acg ttc ctg ctg tgt ctc ccc gtg tcc cag agc tgt    161
41  Leu Ala Ser Leu Thr Phe Leu Leu Cys Leu Pro Val Ser Gln Ser Cys
42  10                  15                  20                  25
44  aac aaa gca ctc tgt gcc agc gat gtg agc aaa tgc ctc att cag gag    209
45  Asn Lys Ala Leu Cys Ala Ser Asp Val Ser Lys Cys Leu Ile Gln Glu
46                  30                  35                  40
48  ctc tgc cag tgc cgg cct gga gaa ggg aac tgc ccc tgc tgt aag gag    257
49  Leu Cys Gln Cys Arg Pro Gly Glu Gly Asn Cys Pro Cys Cys Lys Glu
50                  45                  50                  55
52  tgc atg ctg tgc ctc ggg gcc ctg tgg gac gag tgc tgc gac tgt gtc    305
53  Cys Met Leu Cys Leu Gly Ala Leu Trp Asp Glu Cys Cys Asp Cys Val
54              60                  65                  70
56  ggt atg tgc aac cct cgg aat tac agc gac acc ccg ccc aca tcc aag    353
57  Gly Met Cys Asn Pro Arg Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys
58          75                  80                  85
60  agc acc gtg gag gag ctg cac gag ccc att ccg tcc ctg ttc agg gcg    401
61  Ser Thr Val Glu Glu Leu His Glu Pro Ile Pro Ser Leu Phe Arg Ala
62  90                  95                  100                 105
64  ctg acg gag ggc gac acc cag ctg aac tgg aac atc gtc tcc ttc cct    449
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65 Leu Thr Glu Gly Asp Thr Gln Leu Asn Trp Asn Ile Val Ser Phe Pro
66              110             115             120
68 gtg gca gag gag ctg tca cac cat gaa aac cta gtc tcc ttc cta gaa      497
69 Val Ala Glu Glu Leu Ser His His Glu Asn Leu Val Ser Phe Leu Glu
70              125             130             135
72 act gtg aac cag ctg cac cac caa aac gtg tct gtt ccc agc aac aat      545
73 Thr Val Asn Gln Leu His His Gln Asn Val Ser Val Pro Ser Asn Asn
74              140             145             150
76 gtc cac gcc ccc ttc ccc agc gac aaa gag cgc atg tgc aca gtg gtt      593
77 Val His Ala Pro Phe Pro Ser Asp Lys Glu Arg Met Cys Thr Val Val
78          155             160             165
80 tac ttt gat gac tgc atg tcc atc cac cag tgt aag ata tcc tgc gaa      641
81 Tyr Phe Asp Asp Cys Met Ser Ile His Gln Cys Lys Ile Ser Cys Glu
82 170             175             180             185
84 tcc atg ggt gca tcc aag tat cgc tgg ttt cac aac gcc tgc tgc gag      689
85 Ser Met Gly Ala Ser Lys Tyr Arg Trp Phe His Asn Ala Cys Cys Glu
86              190             195             200
88 tgc atc ggt cca gag tgc att gac tat ggg agt aaa act gtc aag tgt      737
89 Cys Ile Gly Pro Glu Cys Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys
90              205             210             215
92 atg aac tgc atg ttt taaagagggg gaagaaatgc aaaccaaagc agtaagtcat      792
93 Met Asn Cys Met Phe
94          220
96 gaagtgtgca gaaatcttgg ttctggtatg ctaggagtgt gttaagttat atgattgtaa     852
97 ctgtgctttt tatatctggt gcctattagt gtaggtcttt tccattggat tcaatggaac     912
98 tttagtcaca tgaggatcgg gagttcagag gagtcctggg aaaacctgac atgctgacag     972
99 aaggtgccgt cttcttccag ctttccaaac acttctcgtt ttgaacgtga tagcacaagc    1032
100 ctggtacatg tgtggttctc acctgccagt tgtagaacac taggtcccta tagtcacaca   1092
101 tctcttaatt gtgccttggc tggcttacct gttttgtatg agtaaatatt acagtttata   1152
102 attctaacaa ctcacattca agccatgctg aaacttaatt tcaaaccact ttacattggt   1212
103 tttagaaagt aaatatttac tatattttac aacagaagag ttttgcctag ggccagcgag   1272
104 ctgactcagt ggataaaggc gcttgctacc aagcctgata acctgagttc catccccaga   1332
105 gcccgtacag tggaaggaca ggaccagctg ctgggagttg tcctctgacc tccagacagg   1392
106 cacagtatca tgcgtggagg tgtgcttgtg tgtgcacaca cataactaac tgtttttaaa   1452
107 aatataaacc tcttacatgg tgaaatctaa atctgtcgtg tagctctcac actgacagtg   1512
108 gtttggatgt tatgtcccct gtccgcctgt agtgctggtg tggtgagaca cagagtcgtc   1572
109 actgctctgg tatagaagag ttttgtctac caagagtgtc atggcatacc tttggaactt   1632
110 catcaaatgc acttgaggat gacctgggtc aggaagtagc caggtaaaag cagcgggact   1692
111 gtaggcgatg ctccattaga ctccgtgcag agcagcaggt gcacagcata gctgggtgtg   1752
112 cggctgacca ggagagggtc tgactccgca ccagcagaac agcagggtct ccagcacgtg   1812
113 tgggaagcac gtgggagagg gttgaggaag gatgcacaga tgtggacaga gaagcataaa   1872
114 aatgtcggga actcctagta gggtccacct taaaatcgct ttatagtctc tggctttgtt   1932
115 actctgtaag attacacttg tttctggata tctgaatcca aataagcatc atattttaag   1992
116 aagctctgtt tctgaacttc caggggaaa tctgtttaat gtgtttactc ctagcatact    2052
117 acagaatttt ctagctctat agcttcttac ctagcgtttc catagtgctg agcttcatta   2112
118 ctacacgccc ttcctagtaa taaaattctc accttcaagc atgaatcaaa aacaaatatc   2172
119 tataatacac aggttcaatt ttatagaatt gctattttct ctagtgcata tctcattaaa   2232
120 agtaacttttt taggaataat ctttatatgg gtacatattt tggtacataa aatagaaaat   2292
121 gttcttaaac tcattttgta ttatttgaat agttacaaga tgatttgtgg tatcatgggt   2352
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122 acccattata aaccatgctc ttcccagtag ctgacgaact caaggtatca cagccttcta- - 2412
123 agaagccgac ttagaacatg gctgtacatg aatattatac attaaggtgt cctctcactt    2472
124 ctacccagag tgcctctgtt caaaggtgcc ttggaaacat ttcagcccct tccttcttag    2532
125 ctcccacagg gctgtgggtg ttcttgaaat caggaggcgt tttgaaggac cacagctgct    2592
126 ccatttcagc cgctgattct taggaaagtt catgctctga cagaagtgtg ctttgatggc    2652
127 ttctagcggt gcatctcgtc tcgttttctt tgtttgtttt tgttgttgct atcatggttt    2712
128 ggtttggttt tgagacagga tctctgtgca gccctggctg gcctggaatg tactatgtag    2772
129 accaggctgg ctctcctcat gttttcttag tgatggccat aaacattgtt aaaatacatc    2832
130 accatctttt aaaaactttt cattattaaa atttaaaata tagcatgtca ttttttttacc    2892
131 ccatacattt gctatgaaaa attttttaaa ccacctgctt taactttttt attgccctgt    2952
132 ttttcctatt agaattgatc cccactgagg taaatttttat aatcatgttt tgtgtatttt   3012
133 tcctggctcg ccaaggctta tgaagaaata gcagccattc cctgacaggt ttgcgctccc    3072
134 accacagaga ggctgagcaa gatgatcaga ggatcaaggc cagccagagc aaggcactgc    3132
135 ccagaaagca caagtcctgt gctcagcgtt ttgcgtagcg ttttattcct aattgaaatg    3192
136 taatatttca gaagctagca gcctcgctca gtctagacct tccacaccaa tctagcagcg    3252
137 attctcccgt actaaagcct ttgtaagagt ttacggttct tcctcagtga aaaatgatct    3312
138 tgttttttctt acagccggat ccaaagacgc tagatgttaa gggctgaggc tgaagcccgg   3372
139 tgacggggcg ctcacctgtc atggtgcagc cctcgttcca ccgtgagcac cagcaagaga    3432
140 caaacacaag cttgtgagtc agaggccgtt attaaattca tacgcacata ctccctatag    3492
141 cgagacatgg gcttatgggc aggcttttt tttcataaca tttatgagaa aacaatgttt     3552
142 tccccataac atttaattag gactgtagct tattggtaat taaggtacaa aatcaaagtc    3612
143 gagtagaatg tactgttcac acagcgtgtt gtgaaagggg tcctcacacc aaagtttaac    3672
144 tgtaaagttt agaaaaataa cattgtcatt agcatatttg aacacatatt tggaatttct    3732
145 aaaaagcatc aaaatagaaa aagaaagtga aactctggag aatgagatgc tgaagatggg    3792
146 ctatgattta aaggtctgtt ctgtagttag aaagcacctt ttaaagactt tgttcattcc    3852
147 caagagtcta tgttgattgc atttaacatg accgacaact tatatatgta attgtgtaca    3912
148 ttttcattgg ttgtctctgt agtccaaaag aaggtatttt aataaaaaat agaaatgact    3972
149 gtgaaaaaaa aaaa                                                       3986
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152 <211> LENGTH: 222
153 <212> TYPE: PRT
154 <213> ORGANISM: Mus musculus

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160               20                  25                  30
161 Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln Cys Arg Pro Gly
162           35                  40                  45
163 Glu Gly Asn Cys Pro Cys Cys Lys Glu Cys Met Leu Cys Leu Gly Ala
164       50                  55                  60
165 Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys Asn Pro Arg Asn
166 65                  70                  75                  80
167 Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val Glu Glu Leu His
168               85                  90                  95
169 Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu Gly Asp Thr Gln
170               100                 105                 110
171 Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu Glu Leu Ser His
172           115                 120                 125
```

```
173 His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn Gln Leu His His
174     130             135             140
175 Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala Pro Phe Pro Ser
176 145             150             155             160
177 Asp Lys Glu Arg Met Cys Thr Val Val Tyr Phe Asp Asp Cys Met Ser
178             165             170             175
179 Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly Ala Ser Lys Tyr
180             180             185             190
181 Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly Pro Glu Cys Ile
182         195             200             205
183 Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys Met Phe
184     210             215             220
186 <210> SEQ ID NO: 3
187 <211> LENGTH: 19
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
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200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
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208 cgcgcagctg taaacggtag                                             20
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211 <211> LENGTH: 225
212 <212> TYPE: PRT
213 <213> ORGANISM: Drosophila melanogaster
215 <400> SEQUENCE: 5
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217 1               5               10              15
218 Trp Ser Ser Leu Ala Asn Asp Asp Gly Cys Asn Glu Val Val Cys Gly
219             20              25              30
220 Ser Val Val Ser Lys Cys Leu Ile Thr Gln Ser Cys Gln Cys Lys Leu
221         35              40              45
222 Asn Asp Cys His Cys Cys Lys Asp Cys Leu Asn Cys Leu Gly Glu Leu
223     50              55              60
224 Tyr Ile Glu Cys Cys Gly Cys Leu Asp Met Cys Pro Lys His Lys Asp
225 65              70              75              80
226 Val Leu Pro Ser Leu Thr Pro Arg Ser Glu Ile Gly Asp Ile Glu Gly
227             85              90              95
228 Val Pro Glu Leu Phe Asp Thr Leu Thr Ala Glu Asp Asp Glu Gly Trp
229             100             105             110
230 Ser Thr Ile Arg Phe Ser Met Arg Ala Gly Phe Lys Gln Arg Val Gln
231             115             120             125
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232 Gly Gly Ala Ser Gly Asp Ala Gly Asn Gly Asn Gly Asn Gly Asn Ala
233     130                 135                 140
234 Gly Ser Ala Gly Val Thr Leu Cys Thr Val Ile Tyr Val Asn Ser Cys
235 145                 150                 155                 160
236 Ile Arg Ala Asn Lys Cys Arg Gln Gln Cys Glu Ser Met Gly Ala Ser
237                 165                 170                 175
238 Ser Tyr Arg Trp Phe His Asp Gly Cys Cys Glu Cys Val Gly Glu Asn
239                 180                 185                 190
240 Cys Leu Asn Tyr Gly Ile Asn Glu Ser Arg Cys Arg Gly Cys Pro Glu
241             195                 200                 205
242 Asp Gln Asp Gln Leu Leu Thr Ala Asp Thr Val Pro Ala Glu Ala Glu
243         210                 215                 220
244 Gln
245 225
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VERIFICATION SUMMARY   DATE: 06/17/2002
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date